

SEQUENCE LISTING

<110> Chan, Doug W  
 Chen, Ping-Chi B  
 Chen, David J

<120> DNA Dependent Protein Kinase Catalytic Subunit Phosphorylation Sites  
 and Antibodies Thereto

<130> IB-1807 PCT

<140> US 60/375,094

<141> 2003-04-21

<150> US 60/375,094

<151> 2002-04-22

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<170> PatentIn version 3.1

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<212> PRT

<213> Artificial Sequence

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<213> Homo sapiens

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Glu Thr Leu Ser Ala Ala Asp Arg Cys Gly Ala Ala Leu Ala Gly His  
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Gln Leu Ile Arg Gly Leu Gly Gln Glu Cys Val Leu Ser Ser Ser Pro  
35 40 45

Ala Val Leu Ala Leu Gln Thr Ser Leu Val Phe Ser Arg Asp Phe Gly  
50 55 60

Leu Leu Val Phe Val Arg Lys Ser Leu Asn Ser Ile Glu Phe Arg Glu  
65 70 75 80

Cys Arg Glu Glu Ile Leu Lys Phe Leu Cys Ile Phe Leu Glu Lys Met  
85 90 95

Gly Gln Lys Ile Ala Pro Tyr Ser Val Glu Ile Lys Asn Thr Cys Thr  
100 105 110

Ser Val Tyr Thr Lys Asp Arg Ala Ala Lys Cys Lys Ile Pro Ala Leu  
115 120 125

Asp Leu Leu Ile Lys Leu Leu Gln Thr Phe Arg Ser Ser Arg Leu Met  
130 135 140

Asp Glu Phe Lys Ile Gly Glu Leu Phe Ser Lys Phe Tyr Gly Glu Leu  
145 150 155 160

Ala Leu Lys Lys Lys Ile Pro Asp Thr Val Leu Glu Lys Val Tyr Glu  
165 170 175

Leu Leu Gly Leu Leu Gly Glu Val His Pro Ser Glu Met Ile Asn Asn  
180 185 190

Ala Glu Asn Leu Phe Arg Ala Phe Leu Gly Glu Leu Lys Thr Gln Met  
 195 200 205

Thr Ser Ala Val Arg Glu Pro Lys Leu Pro Val Leu Ala Gly Cys Leu  
 210 215 220

Lys Gly Leu Ser Ser Leu Leu Cys Asn Phe Thr Lys Ser Met Glu Glu  
 225 230 235 240

Asp Pro Gln Thr Ser Arg Glu Ile Phe Asn Phe Val Leu Lys Ala Ile  
 245 250 255

Arg Pro Gln Ile Asp Leu Lys Arg Tyr Ala Val Pro Ser Ala Gly Leu  
 260 265 270

Arg Leu Phe Ala Leu His Ala Ser Gln Phe Ser Thr Cys Leu Leu Asp  
 275 280 285

Asn Tyr Val Ser Leu Phe Glu Val Leu Leu Lys Trp Cys Ala His Thr  
 290 295 300

Asn Val Glu Leu Lys Lys Ala Ala Leu Ser Ala Leu Glu Ser Phe Leu  
 305 310 315 320

Lys Gln Val Ser Asn Met Val Ala Lys Asn Ala Glu Met His Lys Asn  
 325 330 335

Lys Leu Gln Tyr Phe Met Glu Gln Phe Tyr Gly Ile Ile Arg Asn Val  
 340 345 350

Asp Ser Asn Asn Lys Glu Leu Ser Ile Ala Ile Arg Gly Tyr Gly Leu  
 355 360 365

Phe Ala Gly Pro Cys Lys Val Ile Asn Ala Lys Asp Val Asp Phe Met  
 370 375 380

Tyr Val Glu Leu Ile Gln Arg Cys Lys Gln Met Phe Leu Thr Gln Thr  
 385 390 395 400

Asp Thr Gly Asp Tyr Arg Val Tyr Gln Met Pro Ser Phe Leu Gln Ser  
 405 410 415

Val Ala Ser Val Leu Leu Tyr Leu Asp Thr Val Pro Glu Val Tyr Thr  
 420 425 430

Pro Val Leu Glu His Leu Val Val Met Gln Ile Asp Ser Phe Pro Gln  
435 440 445

Tyr Ser Pro Lys Met Gln Leu Val Cys Cys Arg Ala Ile Val Lys Val  
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Phe Leu Ala Leu Ala Ala Lys Gly Pro Val Leu Arg Asn Cys Ile Ser  
465 470 475 480

Thr Val Val His Gln Gly Leu Ile Arg Ile Cys Ser Lys Pro Val Val  
485 490 495

Leu Pro Lys Gly Pro Glu Ser Glu Ser Glu Asp His Arg Ala Ser Gly  
500 505 510

Glu Val Arg Thr Gly Lys Trp Lys Val Pro Thr Tyr Lys Asp Tyr Val  
515 520 525

Asp Leu Phe Arg His Leu Leu Ser Ser Asp Gln Met Met Asp Ser Ile  
530 535 540

Leu Ala Asp Glu Ala Phe Phe Ser Val Asn Ser Ser Ser Glu Ser Leu  
545 550 555 560

Asn His Leu Leu Tyr Asp Glu Phe Val Lys Ser Val Leu Lys Ile Val  
565 570 575

Glu Lys Leu Asp Leu Thr Leu Glu Ile Gln Thr Val Gly Glu Gln Glu  
580 585 590

Asn Gly Asp Glu Ala Pro Gly Val Trp Met Ile Pro Thr Ser Asp Pro  
595 600 605

Ala Ala Asn Leu His Pro Ala Lys Pro Lys Asp Phe Ser Ala Phe Ile  
610 615 620

Asn Leu Val Glu Phe Cys Arg Glu Ile Leu Pro Glu Lys Gln Ala Glu  
625 630 635 640

Phe Phe Glu Pro Trp Val Tyr Ser Phe Ser Tyr Glu Leu Ile Leu Gln  
645 650 655

Ser Thr Arg Leu Pro Leu Ile Ser Gly Phe Tyr Lys Leu Leu Ser Ile  
660 665 670

Thr Val Arg Asn Ala Lys Lys Ile Lys Tyr Phe Glu Gly Val Ser Pro  
 675 680 685

Lys Ser Leu Lys His Ser Pro Glu Asp Pro Glu Lys Tyr Ser Cys Phe  
 690 695 700

Ala Leu Phe Val Lys Phe Gly Lys Glu Val Ala Val Lys Met Lys Gln  
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Tyr Lys Asp Glu Leu Leu Ala Ser Cys Leu Thr Phe Leu Leu Ser Leu  
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Pro His Asn Ile Ile Glu Leu Asp Val Arg Ala Tyr Val Pro Ala Leu  
 740 745 750

Gln Met Ala Phe Lys Leu Gly Leu Ser Tyr Thr Pro Leu Ala Glu Val  
 755 760 765

Gly Leu Asn Ala Leu Glu Glu Trp Ser Ile Tyr Ile Asp Arg His Val  
 770 775 780

Met Gln Pro Tyr Tyr Lys Asp Ile Leu Pro Cys Leu Asp Gly Tyr Leu  
 785 790 795 800

Lys Thr Ser Ala Leu Ser Asp Glu Thr Lys Asn Asn Trp Glu Val Ser  
 805 810 815

Ala Leu Ser Arg Ala Ala Gln Lys Gly Phe Asn Lys Val Val Leu Lys  
 820 825 830

His Leu Lys Lys Thr Lys Asn Leu Ser Ser Asn Glu Ala Ile Ser Leu  
 835 840 845

Glu Glu Ile Arg Ile Arg Val Val Gln Met Leu Gly Ser Leu Gly Gly  
 850 855 860

Gln Ile Asn Lys Asn Leu Leu Thr Val Thr Ser Ser Asp Glu Met Met  
 865 870 875 880

Lys Ser Tyr Val Ala Trp Asp Arg Glu Lys Arg Leu Ser Phe Ala Val  
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Pro Phe Arg Glu Met Lys Pro Val Ile Phe Leu Asp Val Phe Leu Pro  
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Arg Val Thr Glu Leu Ala Leu Thr Ala Ser Asp Arg Gln Thr Lys Val

915	920	925
Ala Ala Cys Glu Leu Leu His Ser Met Val Met Phe Met Leu Gly Lys 930 935 940		
Ala Thr Gln Met Pro Glu Gly Gly Gln Gly Ala Pro Pro Met Tyr Gln 945 950 955 960		
Leu Tyr Lys Arg Thr Phe Pro Val Leu Leu Arg Leu Ala Cys Asp Val 965 970 975		
Asp Gln Val Thr Arg Gln Leu Tyr Glu Pro Leu Val Met Gln Leu Ile 980 985 990		
His Trp Phe Thr Asn Asn Lys Lys Phe Glu Ser Gln Asp Thr Val Ser 995 1000 1005		
Leu Leu Glu Ala Ile Leu Asp Gly Ile Val Asp Pro Val Asp Ser 1010 1015 1020		
Thr Leu Arg Asp Phe Cys Gly Arg Cys Ile Arg Glu Phe Leu Lys 1025 1030 1035		
Trp Ser Ile Lys Gln Ile Thr Pro Gln Gln Gln Glu Lys Ser Pro 1040 1045 1050		
Val Asn Thr Lys Ser Leu Phe Lys Arg Leu Tyr Ser Leu Ala Leu 1055 1060 1065		
His Pro Asn Ala Phe Lys Arg Leu Gly Ala Ser Leu Ala Phe Asn 1070 1075 1080		
Asn Ile Tyr Arg Glu Phe Arg Glu Glu Glu Ser Leu Val Glu Gln 1085 1090 1095		
Phe Val Phe Glu Ala Leu Val Ile Tyr Met Glu Ser Leu Ala Leu 1100 1105 1110		
Ala His Ala Asp Glu Lys Ser Leu Gly Thr Ile Gln Gln Cys Cys 1115 1120 1125		
Asp Ala Ile Asp His Leu Cys Arg Ile Ile Glu Lys Lys His Val 1130 1135 1140		
Ser Leu Asn Lys Ala Lys Lys Arg Arg Leu Pro Arg Gly Phe Pro 1145 1150 1155		

Pro Ser Ala Ser Leu Cys Leu Leu Asp Leu Val Lys Trp Leu Leu  
1160 1165 1170

Ala His Cys Gly Arg Pro Gln Thr Glu Cys Arg His Lys Ser Ile  
1175 1180 1185

Glu Leu Phe Tyr Lys Phe Val Pro Leu Leu Pro Gly Asn Arg Ser  
1190 1195 1200

Pro Asn Leu Trp Leu Lys Asp Val Leu Lys Glu Glu Gly Val Ser  
1205 1210 1215

Phe Leu Ile Asn Thr Phe Glu Gly Gly Gly Cys Gly Gln Pro Ser  
1220 1225 1230

Gly Ile Leu Ala Gln Pro Thr Leu Leu Tyr Leu Arg Gly Pro Phe  
1235 1240 1245

Ser Leu Gln Ala Thr Leu Cys Trp Leu Asp Leu Leu Leu Ala Ala  
1250 1255 1260

Leu Glu Cys Tyr Asn Thr Phe Ile Gly Glu Arg Thr Val Gly Ala  
1265 1270 1275

Leu Gln Val Leu Gly Thr Glu Ala Gln Ser Ser Leu Leu Lys Ala  
1280 1285 1290

Val Ala Phe Phe Leu Glu Ser Ile Ala Met His Asp Ile Ile Ala  
1295 1300 1305

Ala Glu Lys Cys Phe Gly Thr Gly Ala Ala Gly Asn Arg Thr Ser  
1310 1315 1320

Pro Gln Glu Gly Glu Arg Tyr Asn Tyr Ser Lys Cys Thr Val Val  
1325 1330 1335

Val Arg Ile Met Glu Phe Thr Thr Thr Leu Leu Asn Thr Ser Pro  
1340 1345 1350

Glu Gly Trp Lys Leu Leu Lys Lys Asp Leu Cys Asn Thr His Leu  
1355 1360 1365

Met Arg Val Leu Val Gln Thr Leu Cys Glu Pro Ala Ser Ile Gly  
1370 1375 1380

Phe	Asn	Ile	Gly	Asp	Val	Gln	Val	Met	Ala	His	Leu	Pro	Asp	Val
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Cys	Val	Asn	Leu	Met	Lys	Ala	Leu	Lys	Met	Ser	Pro	Tyr	Lys	Asp
1400						1405					1410			
Ile	Leu	Glu	Thr	His	Leu	Arg	Glu	Lys	Ile	Thr	Ala	Gln	Ser	Ile
1415						1420					1425			
Glu	Glu	Leu	Cys	Ala	Val	Asn	Leu	Tyr	Gly	Pro	Asp	Ala	Gln	Val
1430						1435					1440			
Asp	Arg	Ser	Arg	Leu	Ala	Ala	Val	Val	Ser	Ala	Cys	Lys	Gln	Leu
1445						1450					1455			
His	Arg	Ala	Gly	Leu	Leu	His	Asn	Ile	Leu	Pro	Ser	Gln	Ser	Thr
1460						1465					1470			
Asp	Leu	His	His	Ser	Val	Gly	Thr	Glu	Leu	Leu	Ser	Leu	Val	Tyr
1475						1480					1485			
Lys	Gly	Ile	Ala	Pro	Gly	Asp	Glu	Arg	Gln	Cys	Leu	Pro	Ser	Leu
1490						1495					1500			
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1505						1510					1515			
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1520						1525					1530			
Asn	Pro	Ala	Val	Leu	Ser	Thr	Ala	Ser	Leu	Gly	Ser	Ser	Gln	Gly
1535						1540					1545			
Ser	Val	Ile	His	Phe	Ser	His	Gly	Glu	Tyr	Phe	Tyr	Ser	Leu	Phe
1550						1555					1560			
Ser	Glu	Thr	Ile	Asn	Thr	Glu	Leu	Leu	Lys	Asn	Leu	Asp	Leu	Ala
1565						1570					1575			
Val	Leu	Glu	Leu	Met	Gln	Ser	Ser	Val	Asp	Asn	Thr	Lys	Met	Val
1580						1585					1590			
Ser	Ala	Val	Leu	Asn	Gly	Met	Leu	Asp	Gln	Ser	Phe	Arg	Glu	Arg
1595						1600					1605			



Ala	Asn	Gln	Lys	His	Gln	Gly	Leu	Lys	Leu	Ala	Thr	Thr	Ile	Leu
1610						1615					1620			
Gln	His	Trp	Lys	Lys	Cys	Asp	Ser	Trp	Trp	Ala	Lys	Asp	Ser	Pro
1625						1630					1635			
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1640						1645					1650			
Gln	Ile	Asp	Ser	Ser	Val	Ser	Phe	Asn	Thr	Ser	His	Gly	Ser	Phe
1655						1660					1665			
Pro	Glu	Val	Phe	Thr	Thr	Tyr	Ile	Ser	Leu	Leu	Ala	Asp	Thr	Lys
1670						1675					1680			
Leu	Asp	Leu	His	Leu	Lys	Gly	Gln	Ala	Val	Thr	Leu	Leu	Pro	Phe
1685						1690					1695			
Phe	Thr	Ser	Leu	Thr	Gly	Gly	Ser	Leu	Glu	Glu	Leu	Arg	Arg	Val
1700						1705					1710			
Leu	Glu	Gln	Leu	Ile	Val	Ala	His	Phe	Pro	Met	Gln	Ser	Arg	Glu
1715						1720					1725			
Phe	Pro	Pro	Gly	Thr	Pro	Arg	Phe	Asn	Asn	Tyr	Val	Asp	Cys	Met
1730						1735					1740			
Lys	Lys	Phe	Leu	Asp	Ala	Leu	Glu	Leu	Ser	Gln	Ser	Pro	Met	Leu
1745						1750					1755			
Leu	Glu	Leu	Met	Thr	Glu	Val	Leu	Cys	Arg	Glu	Gln	Gln	His	Val
1760						1765					1770			
Met	Glu	Glu	Leu	Phe	Gln	Ser	Ser	Phe	Arg	Arg	Ile	Ala	Arg	Arg
1775						1780					1785			
Gly	Ser	Cys	Val	Thr	Gln	Val	Gly	Leu	Leu	Glu	Ser	Val	Tyr	Glu
1790						1795					1800			
Met	Phe	Arg	Lys	Asp	Asp	Pro	Arg	Leu	Ser	Phe	Thr	Arg	Gln	Ser
1805						1810					1815			
Phe	Val	Asp	Arg	Ser	Leu	Leu	Thr	Leu	Leu	Trp	His	Cys	Ser	Leu
1820						1825					1830			
Asp	Ala	Leu	Arg	Glu	Phe	Phe	Ser	Thr	Ile	Val	Val	Asp	Ala	Ile

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Asp Val 1850	Leu Lys Ser Arg Phe 1855	Thr Lys Leu Asn Glu 1860
Asp Thr 1865	Gln Ile Thr Lys Lys 1870	Met Gly Tyr Tyr Lys 1875
Val Met 1880	Tyr Ser Arg Leu Pro 1885	Lys Asp Asp Val His 1890
Ser Lys 1895	Ile Asn Gln Val Phe 1900	His Gly Ser Cys Ile 1905
Asn Glu 1910	Leu Thr Lys Thr Leu 1915	Ile Lys Leu Cys Tyr 1920
Thr Glu 1925	Asn Met Ala Gly Glu 1930	Asn Gln Leu Leu Glu 1935
Leu Tyr 1940	His Cys Ala Ala Tyr 1945	Asn Cys Ala Ile Ser 1950
Cys Val 1955	Phe Asn Glu Leu Lys 1960	Phe Tyr Gln Gly Phe 1965
Glu Lys 1970	Pro Glu Lys Asn Leu 1975	Leu Ile Phe Glu Asn 1980
Leu Lys 1985	Arg Arg Tyr Asn Phe 1990	Pro Val Glu Val Glu 1995
Glu Arg 2000	Lys Lys Lys Tyr Ile 2005	Glu Ile Arg Lys Glu 2010
Ala Ala 2015	Asn Gly Asp Ser Asp 2020	Gly Pro Ser Tyr Met 2025
Ser Tyr 2030	Leu Ala Asp Ser Thr 2035	Leu Ser Glu Glu Met 2040
Asp Phe 2045	Ser Thr Gly Val Gln 2050	Ser Tyr Ser Tyr Ser 2055
Pro Arg 2060	Pro Ala Thr Gly Arg 2065	Phe Arg Arg Arg Glu 2070

Pro Thr	Val His Asp Asp	Val	Leu Glu Leu Glu	Met	Asp Glu Leu
2075		2080		2085	
Asn Arg	His Glu Cys Met	Ala	Pro Leu Thr Ala	Leu	Val Lys His
2090		2095		2100	
Met His	Arg Ser Leu Gly	Pro	Pro Gln Gly Glu	Glu	Asp Ser Val
2105		2110		2115	
Pro Arg	Asp Leu Pro Ser	Trp	Met Lys Phe Leu	His	Gly Lys Leu
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Gly Asn	Pro Ile Val Pro	Leu	Asn Ile Arg Leu	Phe	Leu Ala Lys
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Leu Val	Ile Asn Thr Glu	Glu	Val Phe Arg Pro	Tyr	Ala Lys His
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Trp Leu	Ser Pro Leu Leu	Gln	Leu Ala Ala Ser	Glu	Asn Asn Gly
2165		2170		2175	
Gly Glu	Gly Ile His Tyr	Met	Val Val Glu Ile	Val	Ala Thr Ile
2180		2185		2190	
Leu Ser	Trp Thr Gly Leu	Ala	Thr Pro Thr Gly	Val	Pro Lys Asp
2195		2200		2205	
Glu Val	Leu Ala Asn Arg	Leu	Leu Asn Phe Leu	Met	Lys His Val
2210		2215		2220	
Phe His	Pro Lys Arg Ala	Val	Phe Arg His Asn	Leu	Glu Ile Ile
2225		2230		2235	
Lys Thr	Leu Val Glu Cys	Trp	Lys Asp Cys Leu	Ser	Ile Pro Tyr
2240		2245		2250	
Arg Leu	Ile Phe Glu Lys	Phe	Ser Gly Lys Asp	Pro	Asn Ser Lys
2255		2260		2265	
Asp Asn	Ser Val Gly Ile	Gln	Leu Leu Gly Ile	Val	Met Ala Asn
2270		2275		2280	
Asp Leu	Pro Pro Tyr Asp	Pro	Gln Cys Gly Ile	Gln	Ser Ser Glu
2285		2290		2295	

Tyr	Phe	Gln	Ala	Leu	Val	Asn	Asn	Met	Ser	Phe	Val	Arg	Tyr	Lys
2300						2305					2310			
Glu	Val	Tyr	Ala	Ala	Ala	Ala	Glu	Val	Leu	Gly	Leu	Ile	Leu	Arg
2315						2320					2325			
Tyr	Val	Met	Glu	Arg	Lys	Asn	Ile	Leu	Glu	Glu	Ser	Leu	Cys	Glu
2330						2335					2340			
Leu	Val	Ala	Lys	Gln	Leu	Lys	Gln	His	Gln	Asn	Thr	Met	Glu	Asp
2345						2350					2355			
Lys	Phe	Ile	Val	Cys	Leu	Asn	Lys	Val	Thr	Lys	Ser	Phe	Pro	Pro
2360						2365					2370			
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2375						2380					2385			
Phe	His	Gly	Val	Leu	Lys	Thr	Leu	Cys	Leu	Glu	Val	Val	Leu	Cys
2390						2395					2400			
Arg	Val	Glu	Gly	Met	Thr	Glu	Leu	Tyr	Phe	Gln	Leu	Lys	Ser	Lys
2405						2410					2415			
Asp	Phe	Val	Gln	Val	Met	Arg	His	Arg	Asp	Asp	Glu	Arg	Gln	Lys
2420						2425					2430			
Val	Cys	Leu	Asp	Ile	Ile	Tyr	Lys	Met	Met	Pro	Lys	Leu	Lys	Pro
2435						2440					2445			
Val	Glu	Leu	Arg	Glu	Leu	Leu	Asn	Pro	Val	Val	Glu	Phe	Val	Ser
2450						2455					2460			
His	Pro	Ser	Thr	Thr	Cys	Arg	Glu	Gln	Met	Tyr	Asn	Ile	Leu	Met
2465						2470					2475			
Trp	Ile	His	Asp	Asn	Tyr	Arg	Asp	Pro	Glu	Ser	Glu	Thr	Asp	Asn
2480						2485					2490			
Asp	Ser	Gln	Glu	Ile	Phe	Lys	Leu	Ala	Lys	Asp	Val	Leu	Ile	Gln
2495						2500					2505			
Gly	Leu	Ile	Asp	Glu	Asn	Pro	Gly	Leu	Gln	Leu	Ile	Ile	Arg	Asn
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Phe	Trp	Ser	His	Glu	Thr	Arg	Leu	Pro	Ser	Asn	Thr	Leu	Asp	Arg
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Leu	Leu	Ala	Leu	Asn	Ser	Leu	Tyr	Ser	Pro	Lys	Ile	Glu	Val	His
2540						2545					2550			
Phe	Leu	Ser	Leu	Ala	Thr	Asn	Phe	Leu	Leu	Glu	Met	Thr	Ser	Met
2555						2560					2565			
Ser	Pro	Asp	Tyr	Pro	Asn	Pro	Met	Phe	Glu	His	Pro	Leu	Ser	Glu
2570						2575					2580			
Cys	Glu	Phe	Gln	Glu	Tyr	Thr	Ile	Asp	Ser	Asp	Trp	Arg	Phe	Arg
2585						2590					2595			
Ser	Thr	Val	Leu	Thr	Pro	Met	Phe	Val	Glu	Thr	Gln	Ala	Ser	Gln
2600						2605					2610			
Gly	Thr	Leu	Gln	Thr	Arg	Thr	Gln	Glu	Gly	Ser	Leu	Ser	Ala	Arg
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Trp	Pro	Val	Ala	Gly	Gln	Ile	Arg	Ala	Thr	Gln	Gln	Gln	His	Asp
2630						2635					2640			
Phe	Thr	Leu	Thr	Gln	Thr	Ala	Asp	Gly	Arg	Ser	Ser	Phe	Asp	Trp
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Leu	Thr	Gly	Ser	Ser	Thr	Asp	Pro	Leu	Val	Asp	His	Thr	Ser	Pro
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Ser	Ser	Asp	Ser	Leu	Leu	Phe	Ala	His	Lys	Arg	Ser	Glu	Arg	Leu
2675						2680					2685			
Gln	Arg	Ala	Pro	Leu	Lys	Ser	Val	Gly	Pro	Asp	Phe	Gly	Lys	Lys
2690						2695					2700			
Arg	Leu	Gly	Leu	Pro	Gly	Asp	Glu	Val	Asp	Asn	Lys	Val	Lys	Gly
2705						2710					2715			
Ala	Ala	Gly	Arg	Thr	Asp	Leu	Leu	Arg	Leu	Arg	Arg	Arg	Phe	Met
2720						2725					2730			
Arg	Asp	Gln	Glu	Lys	Leu	Ser	Leu	Met	Tyr	Ala	Arg	Lys	Gly	Val
2735						2740					2745			
Ala	Glu	Gln	Lys	Arg	Glu	Lys	Glu	Ile	Lys	Ser	Glu	Leu	Lys	Met

2750		2755		2760
Lys Gln Asp Ala Gln Val Val	Leu Tyr Arg Ser Tyr Arg His Gly			
2765	2770	2775		
Asp Leu Pro Asp Ile Gln Ile	Lys His Ser Ser Leu Ile Thr Pro			
2780	2785	2790		
Leu Gln Ala Val Ala Gln Arg	Asp Pro Ile Ile Ala Lys Gln Leu			
2795	2800	2805		
Phe Ser Ser Leu Phe Ser Gly	Ile Leu Lys Glu Met Asp Lys Phe			
2810	2815	2820		
Lys Thr Leu Ser Glu Lys Asn	Asn Ile Thr Gln Lys Leu Leu Gln			
2825	2830	2835		
Asp Phe Asn Arg Phe Leu Asn	Thr Thr Phe Ser Phe Phe Pro Pro			
2840	2845	2850		
Phe Val Ser Cys Ile Gln Asp	Ile Ser Cys Gln His Ala Ala Leu			
2855	2860	2865		
Leu Ser Leu Asp Pro Ala Ala	Val Ser Ala Gly Cys Leu Ala Ser			
2870	2875	2880		
Leu Gln Gln Pro Val Gly Ile	Arg Leu Leu Glu Glu Ala Leu Leu			
2885	2890	2895		
Arg Leu Leu Pro Ala Glu Leu	Pro Ala Lys Arg Val Arg Gly Lys			
2900	2905	2910		
Ala Arg Leu Pro Pro Asp Val	Leu Arg Trp Val Glu Leu Ala Lys			
2915	2920	2925		
Leu Tyr Arg Ser Ile Gly Glu	Tyr Asp Val Leu Arg Gly Ile Phe			
2930	2935	2940		
Thr Ser Glu Ile Gly Thr Lys	Gln Ile Thr Gln Ser Ala Leu Leu			
2945	2950	2955		
Ala Glu Ala Arg Ser Asp Tyr	Ser Glu Ala Ala Lys Gln Tyr Asp			
2960	2965	2970		
Glu Ala Leu Asn Lys Gln Asp	Trp Val Asp Gly Glu Pro Thr Glu			
2975	2980	2985		

Ala	Glu	Lys	Asp	Phe	Trp	Glu	Leu	Ala	Ser	Leu	Asp	Cys	Tyr	Asn
2990						2995					3000			
His	Leu	Ala	Glu	Trp	Lys	Ser	Leu	Glu	Tyr	Cys	Ser	Thr	Ala	Ser
3005						3010					3015			
Ile	Asp	Ser	Glu	Asn	Pro	Pro	Asp	Leu	Asn	Lys	Ile	Trp	Ser	Glu
3020						3025					3030			
Pro	Phe	Tyr	Gln	Glu	Thr	Tyr	Leu	Pro	Tyr	Met	Ile	Arg	Ser	Lys
3035						3040					3045			
Leu	Lys	Leu	Leu	Leu	Gln	Gly	Glu	Ala	Asp	Gln	Ser	Leu	Leu	Thr
3050						3055					3060			
Phe	Ile	Asp	Lys	Ala	Met	His	Gly	Glu	Leu	Gln	Lys	Ala	Ile	Leu
3065						3070					3075			
Glu	Leu	His	Tyr	Ser	Gln	Glu	Leu	Ser	Leu	Leu	Tyr	Leu	Leu	Gln
3080						3085					3090			
Asp	Asp	Val	Asp	Arg	Ala	Lys	Tyr	Tyr	Ile	Gln	Asn	Gly	Ile	Gln
3095						3100					3105			
Ser	Phe	Met	Gln	Asn	Tyr	Ser	Ser	Ile	Asp	Val	Leu	Leu	His	Gln
3110						3115					3120			
Ser	Arg	Leu	Thr	Lys	Leu	Gln	Ser	Val	Gln	Ala	Leu	Thr	Glu	Ile
3125						3130					3135			
Gln	Glu	Phe	Ile	Ser	Phe	Ile	Ser	Lys	Gln	Gly	Asn	Leu	Ser	Ser
3140						3145					3150			
Gln	Val	Pro	Leu	Lys	Arg	Leu	Leu	Asn	Thr	Trp	Thr	Asn	Arg	Tyr
3155						3160					3165			
Pro	Asp	Ala	Lys	Met	Asp	Pro	Met	Asn	Ile	Trp	Asp	Asp	Ile	Ile
3170						3175					3180			
Thr	Asn	Arg	Cys	Phe	Phe	Leu	Ser	Lys	Ile	Glu	Glu	Lys	Leu	Thr
3185						3190					3195			
Pro	Leu	Pro	Glu	Asp	Asn	Ser	Met	Asn	Val	Asp	Gln	Asp	Gly	Asp
3200						3205					3210			

Pro	Ser	Asp	Arg	Met	Glu	Val	Gln	Glu	Gln	Glu	Glu	Asp	Ile	Ser
3215						3220					3225			
Ser	Leu	Ile	Arg	Ser	Cys	Lys	Phe	Ser	Met	Lys	Met	Lys	Met	Ile
3230						3235					3240			
Asp	Ser	Ala	Arg	Lys	Gln	Asn	Asn	Phe	Ser	Leu	Ala	Met	Lys	Leu
3245						3250					3255			
Leu	Lys	Glu	Leu	His	Lys	Glu	Ser	Lys	Thr	Arg	Asp	Asp	Trp	Leu
3260						3265					3270			
Val	Ser	Trp	Val	Gln	Ser	Tyr	Cys	Arg	Leu	Ser	His	Cys	Arg	Ser
3275						3280					3285			
Arg	Ser	Gln	Gly	Cys	Ser	Glu	Gln	Val	Leu	Thr	Val	Leu	Lys	Thr
3290						3295					3300			
Val	Ser	Leu	Leu	Asp	Glu	Asn	Asn	Val	Ser	Ser	Tyr	Leu	Ser	Lys
3305						3310					3315			
Asn	Ile	Leu	Ala	Phe	Arg	Asp	Gln	Asn	Ile	Leu	Leu	Gly	Thr	Thr
3320						3325					3330			
Tyr	Arg	Ile	Ile	Ala	Asn	Ala	Leu	Ser	Ser	Glu	Pro	Ala	Cys	Leu
3335						3340					3345			
Ala	Glu	Ile	Glu	Glu	Asp	Lys	Ala	Arg	Arg	Ile	Leu	Glu	Leu	Ser
3350						3355					3360			
Gly	Ser	Ser	Ser	Glu	Asp	Ser	Glu	Lys	Val	Ile	Ala	Gly	Leu	Tyr
3365						3370					3375			
Gln	Arg	Ala	Phe	Gln	His	Leu	Ser	Glu	Ala	Val	Gln	Ala	Ala	Glu
3380						3385					3390			
Glu	Glu	Ala	Gln	Pro	Pro	Ser	Trp	Ser	Cys	Gly	Pro	Ala	Ala	Gly
3395						3400					3405			
Val	Ile	Asp	Ala	Tyr	Met	Thr	Leu	Ala	Asp	Phe	Cys	Asp	Gln	Gln
3410						3415					3420			
Leu	Arg	Lys	Glu	Glu	Glu	Asn	Ala	Ser	Val	Thr	Asp	Ser	Ala	Glu
3425						3430					3435			



Leu	Gln	Ala	Tyr	Pro	Ala	Leu	Val	Val	Glu	Lys	Met	Leu	Lys	Ala
3440						3445					3450			
Leu	Lys	Leu	Asn	Ser	Asn	Glu	Ala	Arg	Leu	Lys	Phe	Pro	Arg	Leu
3455						3460					3465			
Leu	Gln	Ile	Ile	Glu	Arg	Tyr	Pro	Glu	Glu	Thr	Leu	Ser	Leu	Met
3470						3475					3480			
Thr	Lys	Glu	Ile	Ser	Ser	Val	Pro	Cys	Trp	Gln	Phe	Ile	Ser	Trp
3485						3490					3495			
Ile	Ser	His	Met	Val	Ala	Leu	Leu	Asp	Lys	Asp	Gln	Ala	Val	Ala
3500						3505					3510			
Val	Gln	His	Ser	Val	Glu	Glu	Ile	Thr	Asp	Asn	Tyr	Pro	Gln	Ala
3515						3520					3525			
Ile	Val	Tyr	Pro	Phe	Ile	Ile	Ser	Ser	Glu	Ser	Tyr	Ser	Phe	Lys
3530						3535					3540			
Asp	Thr	Ser	Thr	Gly	His	Lys	Asn	Lys	Glu	Phe	Val	Ala	Arg	Ile
3545						3550					3555			
Lys	Ser	Lys	Leu	Asp	Gln	Gly	Gly	Val	Ile	Gln	Asp	Phe	Ile	Asn
3560						3565					3570			
Ala	Leu	Asp	Gln	Leu	Ser	Asn	Pro	Glu	Leu	Leu	Phe	Lys	Asp	Trp
3575						3580					3585			
Ser	Asn	Asp	Val	Arg	Ala	Glu	Leu	Ala	Lys	Thr	Pro	Val	Asn	Lys
3590						3595					3600			
Lys	Asn	Ile	Glu	Lys	Met	Tyr	Glu	Arg	Met	Tyr	Ala	Ala	Leu	Gly
3605						3610					3615			
Asp	Pro	Lys	Ala	Pro	Gly	Leu	Gly	Ala	Phe	Arg	Arg	Lys	Phe	Ile
3620						3625					3630			
Gln	Thr	Phe	Gly	Lys	Glu	Phe	Asp	Lys	His	Phe	Gly	Lys	Gly	Gly
3635						3640					3645			
Ser	Lys	Leu	Leu	Arg	Met	Lys	Leu	Ser	Asp	Phe	Asn	Asp	Ile	Thr
3650						3655					3660			
Asn	Met	Leu	Leu	Leu	Lys	Met	Asn	Lys	Asp	Ser	Lys	Pro	Pro	Gly

3665		3670		3675
Asn Leu Lys Glu Cys Ser Pro Trp Met Ser Asp Phe Lys Val Glu				
3680		3685		3690
Phe Leu Arg Asn Glu Leu Glu Ile Pro Gly Gln Tyr Asp Gly Arg				
3695		3700		3705
Gly Lys Pro Leu Pro Glu Tyr His Val Arg Ile Ala Gly Phe Asp				
3710		3715		3720
Glu Arg Val Thr Val Met Ala Ser Leu Arg Arg Pro Lys Arg Ile				
3725		3730		3735
Ile Ile Arg Gly His Asp Glu Arg Glu His Pro Phe Leu Val Lys				
3740		3745		3750
Gly Gly Glu Asp Leu Arg Gln Asp Gln Arg Val Glu Gln Leu Phe				
3755		3760		3765
Gln Val Met Asn Gly Ile Leu Ala Gln Asp Ser Ala Cys Ser Gln				
3770		3775		3780
Arg Ala Leu Gln Leu Arg Thr Tyr Ser Val Val Pro Met Thr Ser				
3785		3790		3795
Arg Leu Gly Leu Ile Glu Trp Leu Glu Asn Thr Val Thr Leu Lys				
3800		3805		3810
Asp Leu Leu Leu Asn Thr Met Ser Gln Glu Glu Lys Ala Ala Tyr				
3815		3820		3825
Leu Ser Asp Pro Arg Ala Pro Pro Cys Glu Tyr Lys Asp Trp Leu				
3830		3835		3840
Thr Lys Met Ser Gly Lys His Asp Val Gly Ala Tyr Met Leu Met				
3845		3850		3855
Tyr Lys Gly Ala Asn Arg Thr Glu Thr Val Thr Ser Phe Arg Lys				
3860		3865		3870
Arg Glu Ser Lys Val Pro Ala Asp Leu Leu Lys Arg Ala Phe Val				
3875		3880		3885
Arg Met Ser Thr Ser Pro Glu Ala Phe Leu Ala Leu Arg Ser His				
3890		3895		3900

Phe	Ala	Ser	Ser	His	Ala	Leu	Ile	Cys	Ile	Ser	His	Trp	Ile	Leu
3905						3910					3915			
Gly	Ile	Gly	Asp	Arg	His	Leu	Asn	Asn	Phe	Met	Val	Ala	Met	Glu
3920						3925					3930			
Thr	Gly	Gly	Val	Ile	Gly	Ile	Asp	Phe	Gly	His	Ala	Phe	Gly	Ser
3935						3940					3945			
Ala	Thr	Gln	Phe	Leu	Pro	Val	Pro	Glu	Leu	Met	Pro	Phe	Arg	Leu
3950						3955					3960			
Thr	Arg	Gln	Phe	Ile	Asn	Leu	Met	Leu	Pro	Met	Lys	Glu	Thr	Gly
3965						3970					3975			
Leu	Met	Tyr	Ser	Ile	Met	Val	His	Ala	Leu	Arg	Ala	Phe	Arg	Ser
3980						3985					3990			
Asp	Pro	Gly	Leu	Leu	Thr	Asn	Thr	Met	Asp	Val	Phe	Val	Lys	Glu
3995						4000					4005			
Pro	Ser	Phe	Asp	Trp	Lys	Asn	Phe	Glu	Gln	Lys	Met	Leu	Lys	Lys
4010						4015					4020			
Gly	Gly	Ser	Trp	Ile	Gln	Glu	Ile	Asn	Val	Ala	Glu	Lys	Asn	Trp
4025						4030					4035			
Tyr	Pro	Arg	Gln	Lys	Ile	Cys	Tyr	Ala	Lys	Arg	Lys	Leu	Ala	Gly
4040						4045					4050			
Ala	Asn	Pro	Ala	Val	Ile	Thr	Cys	Asp	Glu	Leu	Leu	Leu	Gly	His
4055						4060					4065			
Glu	Lys	Ala	Pro	Ala	Phe	Arg	Asp	Tyr	Val	Ala	Val	Ala	Arg	Gly
4070						4075					4080			
Ser	Lys	Asp	His	Asn	Ile	Arg	Ala	Gln	Glu	Pro	Glu	Ser	Gly	Leu
4085						4090					4095			
Ser	Glu	Glu	Thr	Gln	Val	Lys	Cys	Leu	Met	Asp	Gln	Ala	Thr	Asp
4100						4105					4110			
Pro	Asn	Ile	Leu	Gly	Arg	Thr	Trp	Glu	Gly	Trp	Glu	Pro	Trp	Met
4115						4120					4125			

<210> 4

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD\_RES

<222> (11)..(11)

<223> PHOSPHORYLATION at T2609

<400> 4

Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly  
1 5 10 15

Thr Leu Gln Thr Arg  
20

<210> 5

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD\_RES

<222> (13)..(13)

<223> PHOSPHORYLATION at S2056

<400> 5

Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser Ser Gln Asp Pro  
1 5 10 15

Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln Arg  
20 25

<210> 6

<211> 303

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

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<222> (1)..(303)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (177)..(177)
<223> PHOSPHORYLATION at S2056

<400> 6

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1          5          10          15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
20          25          30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
35          40          45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
50          55          60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu
65          70          75          80

Lys Phe Tyr Gln Gly Phe Leu Phe Ser Glu Lys Pro Glu Lys Asn Leu
85          90          95

Leu Ile Phe Glu Asn Leu Ile Asp Leu Lys Arg Arg Tyr Asn Phe Pro
100         105         110

Val Glu Val Glu Val Pro Met Glu Arg Lys Lys Lys Tyr Ile Glu Ile
115         120         125

Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser
130         135         140

Tyr Met Ser Ser Leu Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu
145         150         155         160

Met Ser Gln Phe Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser
165         170         175

Ser Gln Asp Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln
180         185         190

Arg Asp Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu
195         200         205

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Leu Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His  
 210 215 220

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val Pro  
 225 230 235 240

Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu Gly Asn  
 245 250 255

Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys Leu Val Ile  
 260 265 270

Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His Trp Leu Ser Pro  
 275 280 285

Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly Gly Glu Gly Ile  
 290 295 300

<210> 7

<211> 388

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(388)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD\_RES

<222> (177)..(177)

<223> PHOSPHORYLATION at S2056

<400> 7

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys  
 1 5 10 15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu  
 20 25 30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met  
 35 40 45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala  
 50 55 60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu  
 65 70 75 80

Lys Phe Tyr Gln Gly Phe Leu Phe Ser Glu Lys Pro Glu Lys Asn Leu  
 85 90 95

Leu Ile Phe Glu Asn Leu Ile Asp Leu Lys Arg Arg Tyr Asn Phe Pro  
 100 105 110

Val Glu Val Glu Val Pro Met Glu Arg Lys Lys Lys Tyr Ile Glu Ile  
 115 120 125

Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser  
 130 135 140

Tyr Met Ser Ser Leu Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu  
 145 150 155 160

Met Ser Gln Phe Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser  
 165 170 175

Ser Gln Asp Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln  
 180 185 190

Arg Asp Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu  
 195 200 205

Leu Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His  
 210 215 220

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val Pro  
 225 230 235 240

Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu Gly Asn  
 245 250 255

Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys Leu Val Ile  
 260 265 270

Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His Trp Leu Ser Pro  
 275 280 285

Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly Gly Glu Gly Ile His  
 290 295 300

Tyr Met Val Val Glu Ile Val Ala Thr Ile Leu Ser Trp Thr Gly Leu  
 305 310 315 320

Ala Thr Pro Thr Gly Val Pro Lys Asp Glu Val Leu Ala Asn Arg Leu  
325 330 335

Leu Asn Phe Leu Met Lys His Val Phe His Pro Lys Arg Ala Val Phe  
340 345 350

Arg His Asn Leu Glu Ile Ile Lys Thr Leu Val Glu Cys Trp Lys Asp  
355 360 365

Cys Leu Ser Ile Pro Tyr Arg Leu Ile Phe Glu Lys Phe Ser Gly Lys  
370 375 380

Asp Pro Asn Ser  
385

<210> 8

<211> 821

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(821)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD\_RES

<222> (177)..(177)

<223> PHOSPHORYLATION at S2056

<220>

<221> MOD\_RES

<222> (730)..(730)

<223> PHOSPHORYLATION at T2609

<400> 8

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys  
1 5 10 15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu  
20 25 30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met  
35 40 45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala  
50 55 60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu



65						70						75						80
Lys	Phe	Tyr	Gln	Gly	Phe	Leu	Phe	Ser	Glu	Lys	Pro	Glu	Lys	Asn	Leu			
				85					90					95				
Leu	Ile	Phe	Glu	Asn	Leu	Ile	Asp	Leu	Lys	Arg	Arg	Tyr	Asn	Phe	Pro			
			100					105					110					
Val	Glu	Val	Glu	Val	Pro	Met	Glu	Arg	Lys	Lys	Lys	Tyr	Ile	Glu	Ile			
		115					120					125						
Arg	Lys	Glu	Ala	Arg	Glu	Ala	Ala	Asn	Gly	Asp	Ser	Asp	Gly	Pro	Ser			
	130					135					140							
Tyr	Met	Ser	Ser	Leu	Ser	Tyr	Leu	Ala	Asp	Ser	Thr	Leu	Ser	Glu	Glu			
145					150					155					160			
Met	Ser	Gln	Phe	Asp	Phe	Ser	Thr	Gly	Val	Gln	Ser	Tyr	Ser	Tyr	Ser			
				165					170					175				
Ser	Gln	Asp	Pro	Arg	Pro	Ala	Thr	Gly	Arg	Phe	Arg	Arg	Arg	Glu	Gln			
			180					185						190				
Arg	Asp	Pro	Thr	Val	His	Asp	Asp	Val	Leu	Glu	Leu	Glu	Met	Asp	Glu			
		195					200					205						
Leu	Asn	Arg	His	Glu	Cys	Met	Ala	Pro	Leu	Thr	Ala	Leu	Val	Lys	His			
	210					215					220							
Met	His	Arg	Ser	Leu	Gly	Pro	Pro	Gln	Gly	Glu	Glu	Asp	Ser	Val	Pro			
225					230					235					240			
Arg	Asp	Leu	Pro	Ser	Trp	Met	Lys	Phe	Leu	His	Gly	Lys	Leu	Gly	Asn			
				245					250					255				
Pro	Ile	Val	Pro	Leu	Asn	Ile	Arg	Leu	Phe	Leu	Ala	Lys	Leu	Val	Ile			
			260					265					270					
Asn	Thr	Glu	Glu	Val	Phe	Arg	Pro	Tyr	Ala	Lys	His	Trp	Leu	Ser	Pro			
		275					280					285						
Leu	Leu	Gln	Leu	Ala	Ala	Ser	Glu	Asn	Asn	Gly	Gly	Glu	Gly	Ile	His			
	290					295					300							
Tyr	Met	Val	Val	Glu	Ile	Val	Ala	Thr	Ile	Leu	Ser	Trp	Thr	Gly	Leu			
305					310					315					320			

Ala Thr Pro Thr Gly Val Pro Lys Asp Glu Val Leu Ala Asn Arg Leu  
 325 330 335

Leu Asn Phe Leu Met Lys His Val Phe His Pro Lys Arg Ala Val Phe  
 340 345 350

Arg His Asn Leu Glu Ile Ile Lys Thr Leu Val Glu Cys Trp Lys Asp  
 355 360 365

Cys Leu Ser Ile Pro Tyr Arg Leu Ile Phe Glu Lys Phe Ser Gly Lys  
 370 375 380

Asp Pro Asn Ser Lys Asp Asn Ser Val Gly Ile Gln Leu Leu Gly Ile  
 385 390 395 400

Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro Gln Cys Gly Ile Gln  
 405 410 415

Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn Met Ser Phe Val Arg  
 420 425 430

Tyr Lys Glu Val Tyr Ala Ala Ala Ala Glu Val Leu Gly Leu Ile Leu  
 435 440 445

Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu Glu Ser Leu Cys Glu  
 450 455 460

Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn Thr Met Glu Asp Lys  
 465 470 475 480

Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser Phe Pro Pro Leu Ala  
 485 490 495

Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu Pro Lys Phe His Gly  
 500 505 510

Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu Cys Arg Val Glu Gly  
 515 520 525

Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys Asp Phe Val Gln Val  
 530 535 540

Met Arg His Arg Asp Asp Glu Arg Gln Lys Val Cys Leu Asp Ile Ile  
 545 550 555 560

Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu Leu Arg Glu Leu Leu  
 565 570 575

Asn Pro Val Val Glu Phe Val Ser His Pro Ser Thr Thr Cys Arg Glu  
 580 585 590

Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp Asn Tyr Arg Asp Pro  
 595 600 605

Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile Phe Lys Leu Ala Lys  
 610 615 620

Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly Leu Gln Leu  
 625 630 635 640

Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro Ser Asn Thr  
 645 650 655

Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro Lys Ile Glu  
 660 665 670

Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu Met Thr Ser  
 675 680 685

Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro Leu Ser Glu  
 690 695 700

Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg Phe Arg Ser  
 705 710 715 720

Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly Thr  
 725 730 735

Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg Trp Pro Val  
 740 745 750

Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe Thr Leu Thr  
 755 760 765

Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser  
 770 775 780

Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp Ser Leu Leu  
 785 790 795 800

Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro Leu Lys Ser  
805 810 815

Val Gly Pro Asp Phe  
820

<210> 9

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(440)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD\_RES

<222> (349)..(349)

<223> PHOSPHORYLATION at T2609

<400> 9

Ser Gly Lys Asp Pro Asn Ser Lys Asp Asn Ser Val Gly Ile Gln Leu  
1 5 10 15

Leu Gly Ile Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro Gln Cys  
20 25 30

Gly Ile Gln Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn Met Ser  
35 40 45

Phe Val Arg Tyr Lys Glu Val Tyr Ala Ala Ala Ala Glu Val Leu Gly  
50 55 60

Leu Ile Leu Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu Glu Ser  
65 70 75 80

Leu Cys Glu Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn Thr Met  
85 90 95

Glu Asp Lys Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser Phe Pro  
100 105 110

Pro Leu Ala Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu Pro Lys  
115 120 125

Phe His Gly Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu Cys Arg  
130 135 140

Val Glu Gly Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys Asp Phe  
145 150 155 160

Val Gln Val Met Arg His Arg Asp Asp Glu Arg Gln Lys Val Cys Leu  
165 170 175

Asp Ile Ile Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu Leu Arg  
180 185 190

Glu Leu Leu Asn Pro Val Val Glu Phe Val Ser His Pro Ser Thr Thr  
195 200 205

Cys Arg Glu Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp Asn Tyr  
210 215 220

Arg Asp Pro Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile Phe Lys  
225 230 235 240

Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly  
245 250 255

Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro  
260 265 270

Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro  
275 280 285

Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu  
290 295 300

Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro  
305 310 315 320

Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg  
325 330 335

Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser  
340 345 350

Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg  
355 360 365

Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe  
370 375 380

Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr  
 385 390 395 400

Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp  
 405 410 415

Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro  
 420 425 430

Leu Lys Ser Val Gly Pro Asp Phe  
 435 440

<210> 10  
 <211> 200  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> PEPTIDE  
 <222> (1)..(200)  
 <223> HUMAN GENETIC ORIGIN

<220>  
 <221> MOD\_RES  
 <222> (109)..(109)  
 <223> PHOSPHORYLATION at T2609

<400> 10

Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly  
 1 5 10 15

Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro  
 20 25 30

Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro  
 35 40 45

Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu  
 50 55 60

Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro  
 65 70 75 80

Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg  
 85 90 95

Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser  
 100 105 110

Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg  
 115 120 125

Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe  
 130 135 140

Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr  
 145 150 155 160

Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp  
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Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro  
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Leu Lys Ser Val Gly Pro Asp Phe  
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<210> 11

<211> 428

<212> PRT

<213> Artificial Sequence

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<222> (1)..(428)

<223> HUMAN GENETIC ORIGIN

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<221> MOD\_RES

<222> (335)..(335)

<223> PHOSPHORYLATION at T2609

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Gln Leu Leu Gly Ile Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro  
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Gln Cys Gly Ile Gln Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn  
 20 25 30

Met Ser Phe Val Arg Tyr Lys Glu Val Tyr Ala Ala Ala Ala Glu Val  
 35 40 45

Leu Gly Leu Ile Leu Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu  
 50 55 60

Glu Ser Leu Cys Glu Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn  
 65 70 75 80

Thr Met Glu Asp Lys Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser  
 85 90 95

Phe Pro Pro Leu Ala Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu  
 100 105 110

Pro Lys Phe His Gly Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu  
 115 120 125

Cys Arg Val Glu Gly Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys  
 130 135 140

Asp Phe Val Gln Val Met Arg His Arg Asp Asp Glu Arg Gln Lys Val  
 145 150 155 160

Cys Leu Asp Ile Ile Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu  
 165 170 175

Leu Arg Glu Leu Leu Asn Pro Val Val Glu Phe Val Ser His Pro Ser  
 180 185 190

Thr Thr Cys Arg Glu Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp  
 195 200 205

Asn Tyr Arg Asp Pro Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile  
 210 215 220

Phe Lys Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn  
 225 230 235 240

Pro Gly Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg  
 245 250 255

Leu Pro Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr  
 260 265 270

Ser Pro Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu  
 275 280 285

Leu Glu Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu  
 290 295 300

His Pro Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp  
 305 310 315 320



Trp Arg Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln  
325 330 335

Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser  
340 345 350

Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His  
355 360 365

Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp  
370 375 380

Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser  
385 390 395 400

Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg  
405 410 415

Ala Pro Leu Lys Ser Val Gly Pro Asp Phe Gly Lys  
420 425

<210> 12

<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(273)

<223> HUMAN GENETIC ORIGIN

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<221> MOD\_RES

<222> (180)..(180)

<223> PHOSPHORYLATION at T2609

<400> 12

Glu Arg Gln Lys Val Cys Leu Asp Ile Ile Tyr Lys Met Met Pro Lys  
1 5 10 15

Leu Lys Pro Val Glu Leu Arg Glu Leu Leu Asn Pro Val Val Glu Phe  
20 25 30

Val Ser His Pro Ser Thr Thr Cys Arg Glu Gln Met Tyr Asn Ile Leu  
35 40 45

Met Trp Ile His Asp Asn Tyr Arg Asp Pro Glu Ser Glu Thr Asp Asn  
50 55 60

Asp Ser Gln Glu Ile Phe Lys Leu Ala Lys Asp Val Leu Ile Gln Gly  
65 70 75 80

Leu Ile Asp Glu Asn Pro Gly Leu Gln Leu Ile Ile Arg Asn Phe Trp  
85 90 95

Ser His Glu Thr Arg Leu Pro Ser Asn Thr Leu Asp Arg Leu Leu Ala  
100 105 110

Leu Asn Ser Leu Tyr Ser Pro Lys Ile Glu Val His Phe Leu Ser Leu  
115 120 125

Ala Thr Asn Phe Leu Leu Glu Met Thr Ser Met Ser Pro Asp Tyr Pro  
130 135 140

Asn Pro Met Phe Glu His Pro Leu Ser Glu Cys Glu Phe Gln Glu Tyr  
145 150 155 160

Thr Ile Asp Ser Asp Trp Arg Phe Arg Ser Thr Val Leu Thr Pro Met  
165 170 175

Phe Val Glu Thr Gln Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln  
180 185 190

Glu Gly Ser Leu Ser Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala  
195 200 205

Thr Gln Gln Gln His Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg  
210 215 220

Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp  
225 230 235 240

His Thr Ser Pro Ser Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser  
245 250 255

Glu Arg Leu Gln Arg Ala Pro Leu Lys Ser Val Gly Pro Asp Phe Gly  
260 265 270

Lys

<210> 13

<211> 140

<212> PRT  
<213> Artificial Sequence

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<223> PHOSPHORYLATION at T2609

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Phe Leu Leu Glu Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met  
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Phe Glu His Pro Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp  
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Ser Asp Trp Arg Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu  
35 40 45

Thr Gln Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser  
50 55 60

Leu Ser Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln  
65 70 75 80

Gln His Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe  
85 90 95

Asp Trp Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser  
100 105 110

Pro Ser Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu  
115 120 125

Gln Arg Ala Pro Leu Lys Ser Val Gly Pro Asp Phe  
130 135 140

<210> 14

<211> 102  
<212> PRT  
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<223> HUMAN GENETIC ORIGIN

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 <223> PHOSPHORYLATION at T2609

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Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly Thr Leu  
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Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg Trp Pro Val Ala  
 20 25 30

Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe Thr Leu Thr Gln  
 35 40 45

Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser Thr  
 50 55 60

Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp Ser Leu Leu Phe  
 65 70 75 80

Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro Leu Lys Ser Val  
 85 90 95

Gly Pro Asp Phe Gly Lys  
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<210> 15

<211> 13509

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (6233)..(6235)

<223> Encodes S2056

<220>

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<222> (7882)..(7884)

<223> Encodes T2609

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<223> HUMAN GENETIC ORIGIN

<220>

<221> misc\_feature

<222> (31)..(33)

<223> encodes T2609 residue

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<213> Artificial sequence

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<223> HUMAN GENETIC ORIGIN

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<222> (37)..(37)

<223> encodes S2056 residue

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ggtcggttttc ggagacggga gcagcgg 87

<210> 18

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<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (1)..(909)

<223> HUMAN GENETIC ORIGIN

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<221> misc\_feature

<222> (529)..(529)

<223> encodes S2056 residue

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tacgatgcat ttacagagaa catggcagga gagaatcagc tgctggagag gagaagactt 180

taccattgtg cagcatacaa ctgcgccata tctgtcatct gctgtgtctt caatgagtta 240

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<210> 19

<211> 1164
<212> DNA
<213> Artificial sequence

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<222> (1)..(1164)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (529)..(531)
<223> encodes S2056 residue

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1164

<210> 20

<211> 2463

<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (1)..(2463)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc\_feature

<222> (529)..(531)

<223> encodes S2056 residue

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<221> misc\_feature

<222> (2188)..(2190)

<223> encodes T2609 residue

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tacgatgcat ttacagagaa catggcagga gagaatcagc tgctggagag gagaagactt	180
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<212> DNA

<213> Artificial sequence

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<223> cDNA sequence encoding the 2261-2700 peptide

<220>

<221> CDS

<222> (1)..(1320)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc\_feature

<222> (1045)..(1047)

<223> encodes T2609 residue

<400> 21

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<220>  
 <223> cDNA sequence encoding the 2500-2700 peptide

<220>  
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 <222> (1)..(600)  
 <223> HUMAN GENETIC ORIGIN

<220>  
 <221> misc\_feature  
 <222> (325)..(327)  
 <223> encodes T2609 residue

<400> 22

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ttggcaaaag atgtgctgat tcaaggattg atcgatgaga accctggact tcaattaatt      60
attcgaaaatt tctggagcca tgaaactagg ttaccttcaa ataccttgga cgggttgctg    120
gcactaaatt ccttatattc tcctaagata gaagtgcact ttttaagttt agcaacaaat    180
tttctgctcg aaatgaccag catgagccca gattatccaa accccatggt cgagcatcct    240
ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcgttt ccgaagtact    300
gttctcactc cgatgtttgt ggagaccag gcctcccagg gcactctcca gaccctgacc    360
caggaagggt ccctctcagc tcgctggcca gtggcagggc agataagggc caccagcag    420
cagcatgact tcacactgac acagactgca gatggaagaa gtcatttga ttggctgacc    480
gggagcagca ctgaccgct ggtcgaccac accagtcctt catctgactc cttgctgttt    540
gccacaaga ggagtgaag gttacagaga gcacccttga agtcagtggg gcctgatttt    600

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<210> 23

<211> 1284  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> cDNA sequence encoding 2275-2702 peptide

<220>  
 <221> CDS  
 <222> (1)..(1284)  
 <223> HUMAN GENETIC ORIGIN

<220>  
 <221> misc\_feature  
 <222> (1003)..(1005)  
 <223> encodes T2609 residue

<400> 23

caattgctag gcatcgtgat ggccaatgac ctgcctccct atgacccaca gtgtggcatc	60
cagagtagcg aatacttcca ggctttggtg aataatatgt cttttgtaag atataaagaa	120
gtgtatgccg ctgcagcaga agttctagga cttatacttc gatatgttat ggagagaaaa	180
aacatactgg aggagtctct gtgtgaactg gttgcgaaac aattgaagca acatcagaat	240
actatggagg acaagtttat tgtgtgcttg aacaaagtga ccaagagctt ccctcctctt	300
gcagacaggt tcatgaatgc tgtgttcttt ctgctgccaa aatttcatgg agtggtgaaa	360
acactctgtc tggagggtgt actttgtcgt gtggagggaa tgacagagct gtacttccag	420
ttaaagagca aggacttcgt tcaagtcatg agacatagag atgatgaaag aaaaaagta	480
tgtttggaca taatttataa gatgatgcc aagttaaaac cagtagaact ccgagaactt	540
ctgaaccccg ttgtggaatt cgtttcccat ctttctacaa catgtaggga acaaatgtat	600
aatattctca tgtggattca tgataattac agagatccag aaagtgcagc agataatgac	660
tcccaggaaa tatttaagtt ggcaaaagat gtgctgattc aaggattgat cgatgagaac	720
cctggacttc aattaattat tcgaaatttc tggagccatg aaactagggt accttcaa	780
accttggacc ggttgctggc actaaattcc ttatattctc ctaagataga agtgcacttt	840
ttaagtttag caacaaattt tctgctcgaa atgaccagca tgagcccaga ttatccaaac	900
cccatgttcg agcatcctct gtcagaatgc gaatttcagg aatataccat tgattctgat	960
tggcgtttcc gaagtactgt tctcactccg atgtttgtgg agaccaggc ctcccagggc	1020
actctccaga cccgtaccca ggaaggggtc ctctcagctc gctggccagt ggcagggcag	1080
ataagggcca cccagcagca gcatgacttc aactgcacac agactgcaga tggaagaagc	1140
tcatttgatt ggctgaccgg gagcagcact gacccgctgg tcgaccacac cagtccttca	1200
tctgactcct tgctgtttgc ccacaagagg agtgaaaggt tacagagagc acccttgaag	1260
tcagtggggc ctgatttttg gaaa	1284

<210> 24

<211> 819

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence encoding 2429-2072 peptide

<220>

<221> CDS

<222> (1)..(819)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc\_feature

<222> (538)..(540)  
 <223> encodes T2609 residue

<400> 24

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gaaagacaaa aagtatgttt ggacataatt tataagatga tgccaaagtt aaaaccagta      60
gaactccgag aactttctgaa ccccgttgtg gaattcgttt cccatccttc tacaacatgt      120
agggaacaaa tgtataatat tctcatgtgg attcatgata attacagaga tccagaaagt      180
gagacagata atgactccca ggaaatatat aagttggcaa aagatgtgct gattcaagga      240
ttgatcgatg agaaccctgg acttcaatta attattcgaa atttctggag ccatgaaact      300
aggttacctt caaatacctt ggaccgggtg ctggcactaa attccttata ttctcctaag      360
atagaagtgc actttttaag tttagcaaca aattttctgc tcgaaatgac cagcatgagc      420
ccagattatc caaaccctat gttcgagcat cctctgtcag aatgcgaatt tcaggaatat      480
accattgatt ctgattggcg tttccgaagt actgttctca ctccgatgtt tgtggagacc      540
caggcctccc agggcactct ccagaccctg acccaggaag ggtccctctc agctcgctgg      600
ccagtggcag ggcagataag ggccaccag cagcagcatg acttcacact gacacagact      660
gcagatggaa gaagctcatt tgattggctg accgggagca gactgaccc gctggctgac      720
cacaccagtc ctcactctga ctcttctgtg tttgccaca agaggagtga aaggttacag      780
agagcaccct tgaagtcagt ggggcctgat tttgggaaa      819
  
```

<210> 25

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA Sequence encoding 2561-2700 peptide

<220>

<221> CDS

<222> (1)..(420)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc\_feature

<222> (145)..(147)

<223> Encodes T2609 residue

<400> 25

```

tttctgctcg aaatgaccag catgagccca gattatccaa accccatgtt cgagcatcct      60
ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcgttt ccgaagtact      120
gttctcactc cgatgtttgt ggagaccag gcctcccagg gcactctcca gaccctgacc      180
  
```

caggaagggt ccctctcagc tcgctggcca gtggcagggc agataagggc caccagcag 240  
cagcatgact tcacactgac acagactgca gatggaagaa gctcatttga ttggctgacc 300  
gggagcagca ctgacccgct ggtcgaccac accagtcctt catctgactc cttgctgttt 360  
gcccacaaga ggagtgaaag gttacagaga gcacccttga agtcagtggg gcctgatttt 420

<210> 26

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence encoding 2600-2702 peptide

<220>

<221> CDS

<222> (1)..(306)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc\_feature

<222> (25)..(27)

<223> Encodes T2609 residue

<400> 26

gttctcactc cgatgtttgt ggagaccag gcctcccagg gcactctcca gaccggtacc 60  
caggaagggt ccctctcagc tcgctggcca gtggcagggc agataagggc caccagcag 120  
cagcatgact tcacactgac acagactgca gatggaagaa gctcatttga ttggctgacc 180  
gggagcagca ctgacccgct ggtcgaccac accagtcctt catctgactc cttgctgttt 240  
gcccacaaga ggagtgaaag gttacagaga gcacccttga agtcagtggg gcctgatttt 300  
gggaaa 306

<210> 27

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Primer to create T2609A mutation

<400> 27

tccgatgttt gtggaggacc aggcctccca gggc 34

<210> 28

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse primer to create T2609A mutation

<400> 28

gccctgggag gcctgggcct ccacaaacat cgga

34